The shift toward yearling smolts in Snake River fall Chinook salmon:

Evolution or phenotypic plasticity?

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Life history changes in Snake River fall Chinook salmon

Historically, ~100% subyearling migrants

Today:

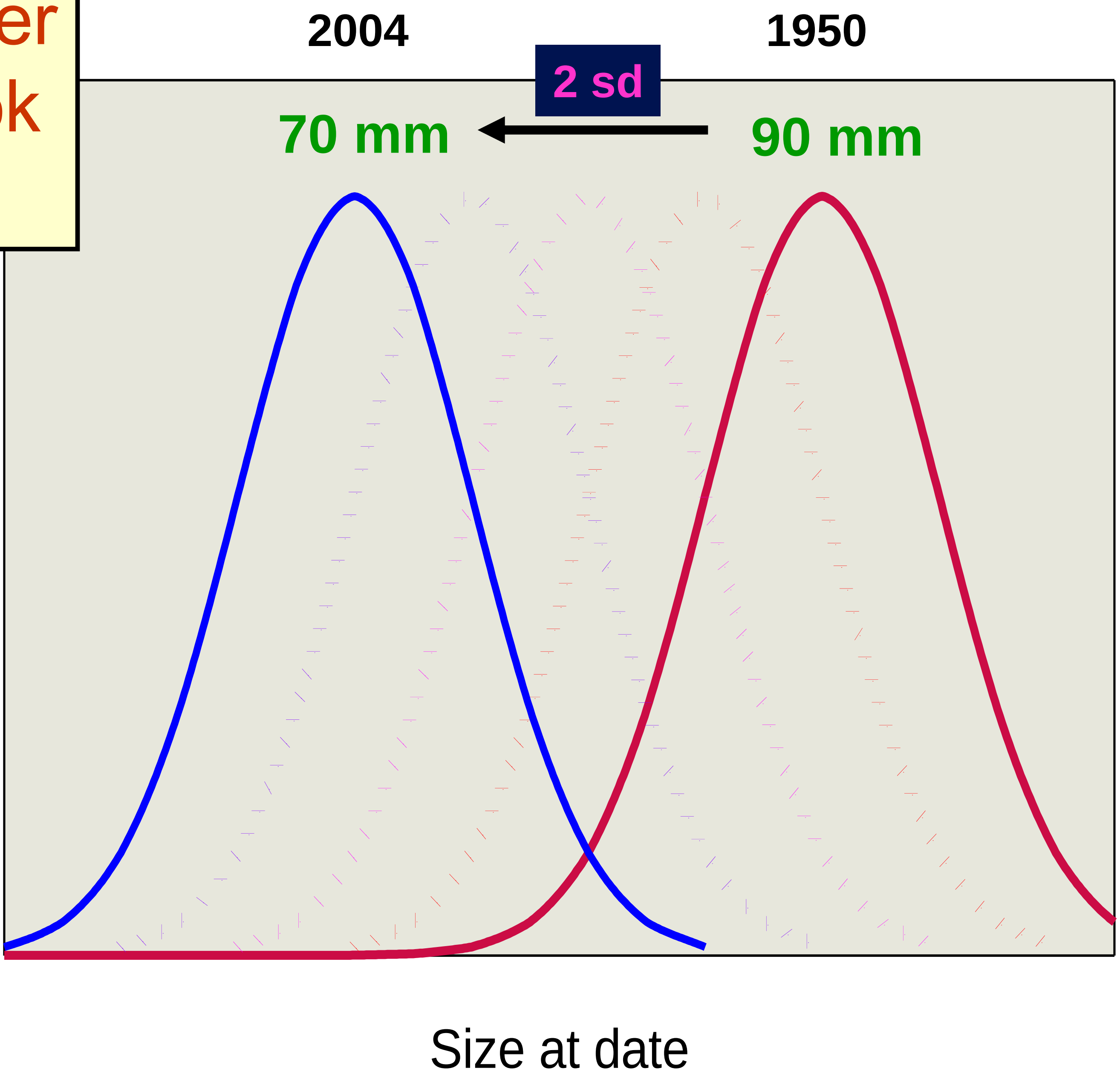
~23% of migrants are yearlings

~44% of adult returns now come from yearling migrants

→ Positive selection favoring yearling life history?

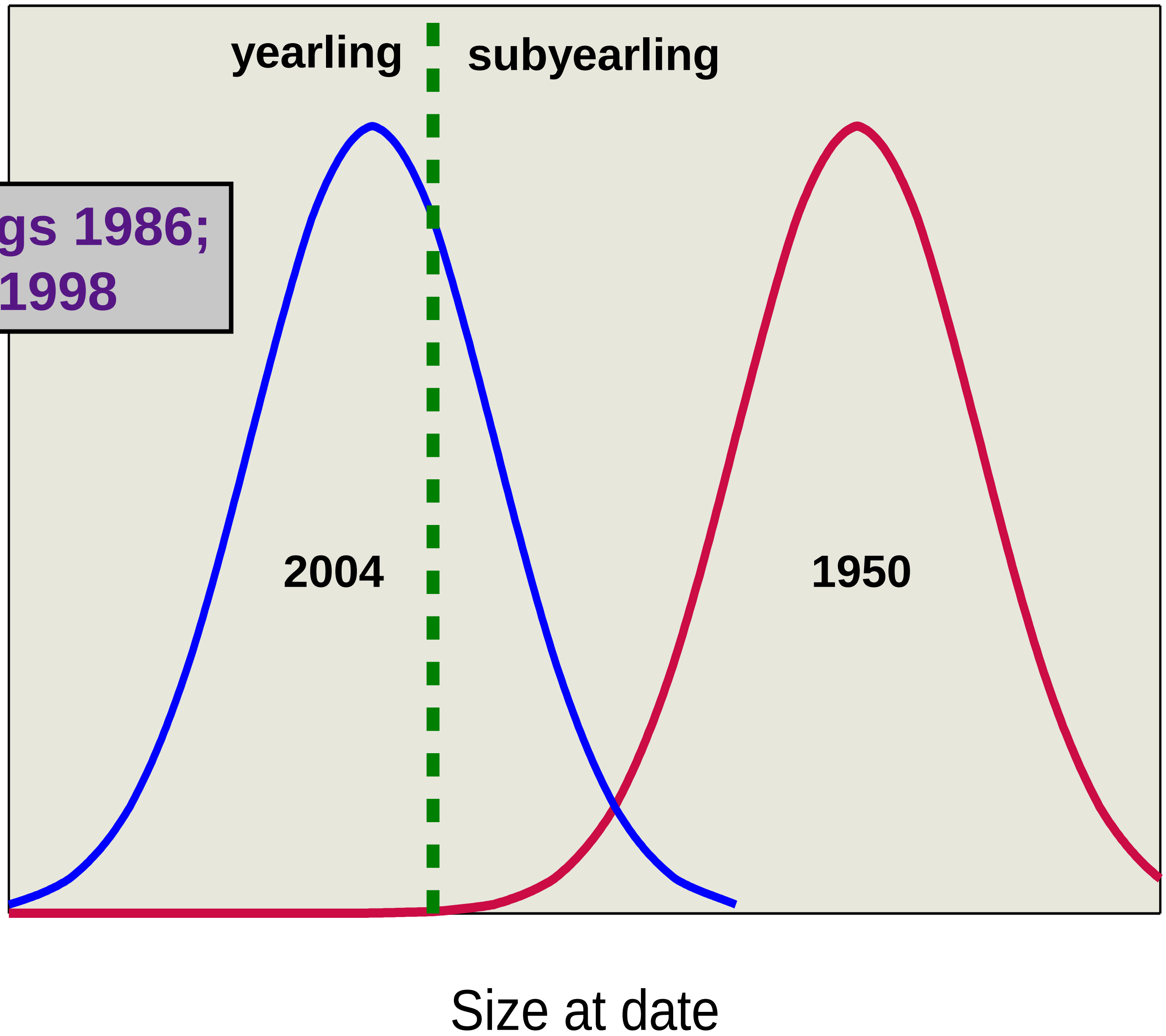
Williams et al. 2008
Evol Apps

Snake River fall chinook salmon



B. Connor Unpubl. data

Threshold for smolting



Myers & Hutchings 1986;
Thorpe et al. 1998

Rate of phenotypic change:
2 sd in 50 years = 12 generations

Can it be explained by drift?

No – would require N_e ~ 10 (est N_e ~ 1000)

Can it be explained by evolution?

Yes – required evolutionary rate falls within empirical range (assuming h^2 = 0.4)

Can it be explained by environmental changes and phenotypic plasticity?

Perhaps – but no quantitative analysis

Stevan Arnold model (after Lande 1976)

So what?

What happens if they take out the dams?

- If it's only phenotypic plasticity, no problem
- If evolution is involved, population could be maladapted to its restored ecosystem

→ Importance of maintaining genetic diversity for smolt age

Methods

Spawning matrix of known crosses with life history and biological information (Nez Perce Tribal Hatchery, Lapwai, ID)

Parentage analysis to correlate parent and offspring life history

- All parents and juvenile offspring genotyped at 11 microsatellite loci (2007-2009)
- Random sample of offspring taken at different rearing sites at PIT-tagging
- Juvenile growth rate as a proxy for smolt age

Hypothesis

If life history shift has a genetic basis:

- Juvenile life history of parents should predict juvenile life history of offspring
- Parents who were subyearling should produce faster growing offspring (proxy for subyearling smolts)

Three major analyses

- Linear models and ANOVA to assess importance of parental life history for juvenile growth rate
- Relating migration data (PITtags) to parental life history and juvenile growth rate
- Animal model to estimate heritability of growth rate

Response variable: Juvenile growth rate

Potential explanatory variable: Parental life history (smolt age)

Covariates: Site, year, parental size, parental origin (H or W)

Sites

Nez Perce Hatchery

Parental Life Histories

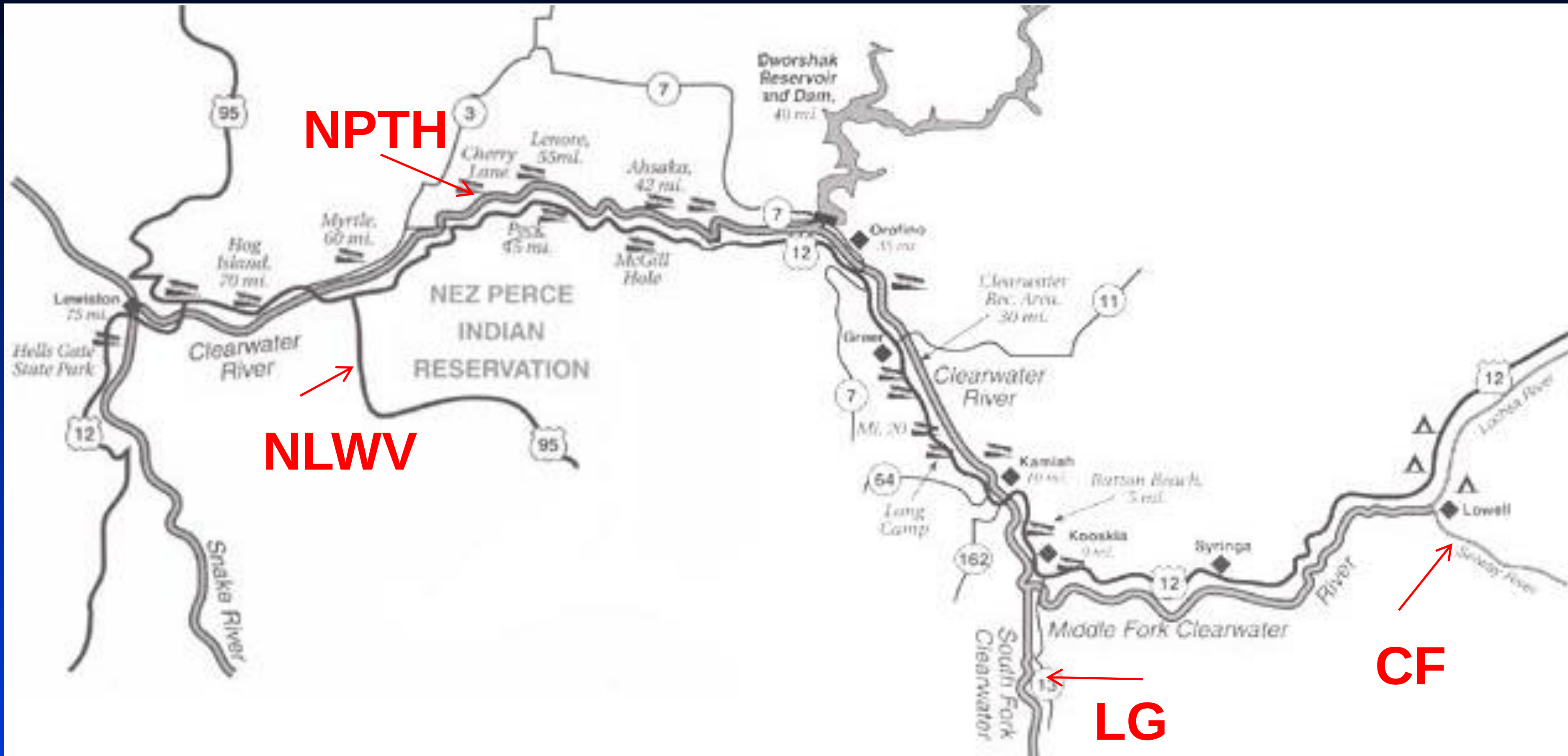
Subyearling
Yearling
Forced yearling

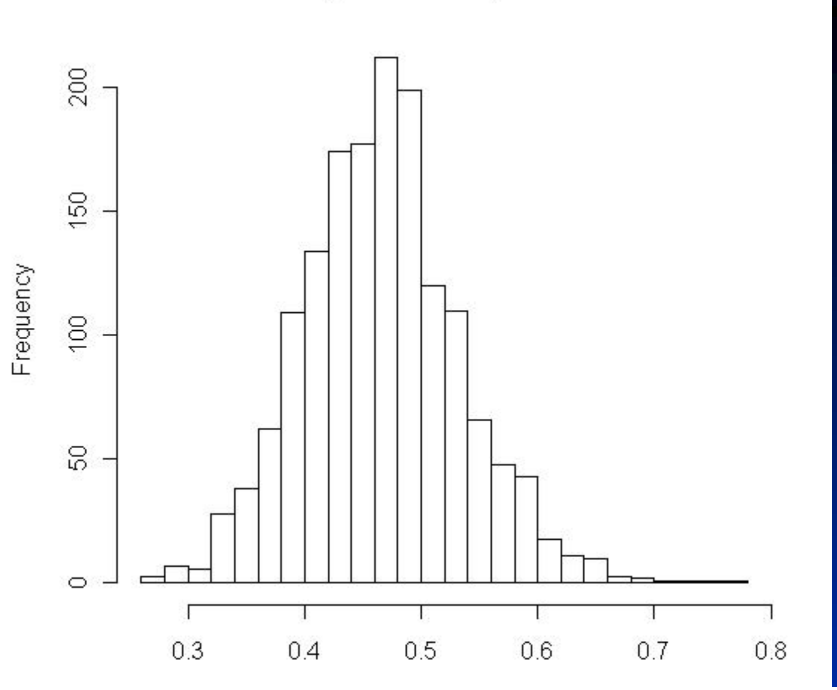
Brood year 2007

Site	Parental crosses	Tissue	DNA	Assigned
N. Lapwai	52			
N. pond	102	571	250	150
S. pond	77	434	250	200
Luke's Guch	38	1000	250	240
Cedar Flats	38	1000	250	238

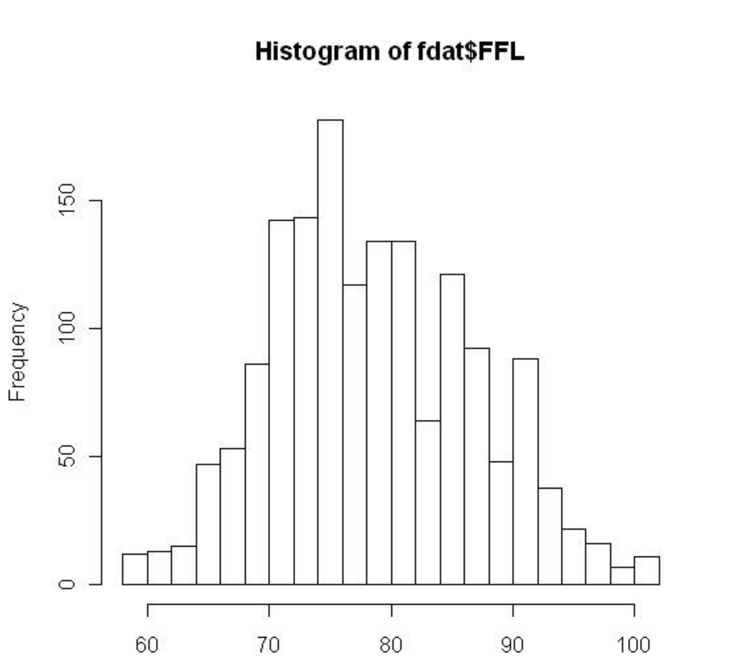
Tissues / DNA

Total	Parents	Juveniles
	574	828

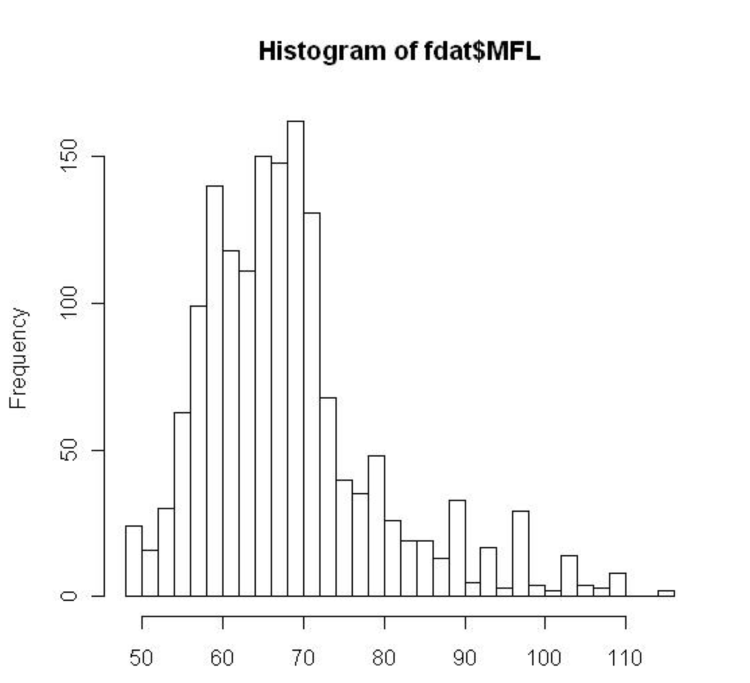

NPTH
NLWV
LG
CF
Dworshak Reservoir and Dam, 40 mi.
Cherry Lane
Lenore, 55mi.
Ahsaka, 42 mi.
Myrtle, 60 mi.
Hog Island, 70 mi.
Peck 45 mi.
McGill Hole
Lewiston 75 mi.
Hells Gate State Park
Clearwater River
NEZ PERCE INDIAN RESERVATION
Orofino
Clearwater Rec. Area 30 mi.
Greer
Kamiah
Long Camp
Kooskia
Syringa
Lowell
Middle Fork Clearwater River
South Fork Clearwater
Snake River
95
3
7
12
11
54
162
13



Growth rate

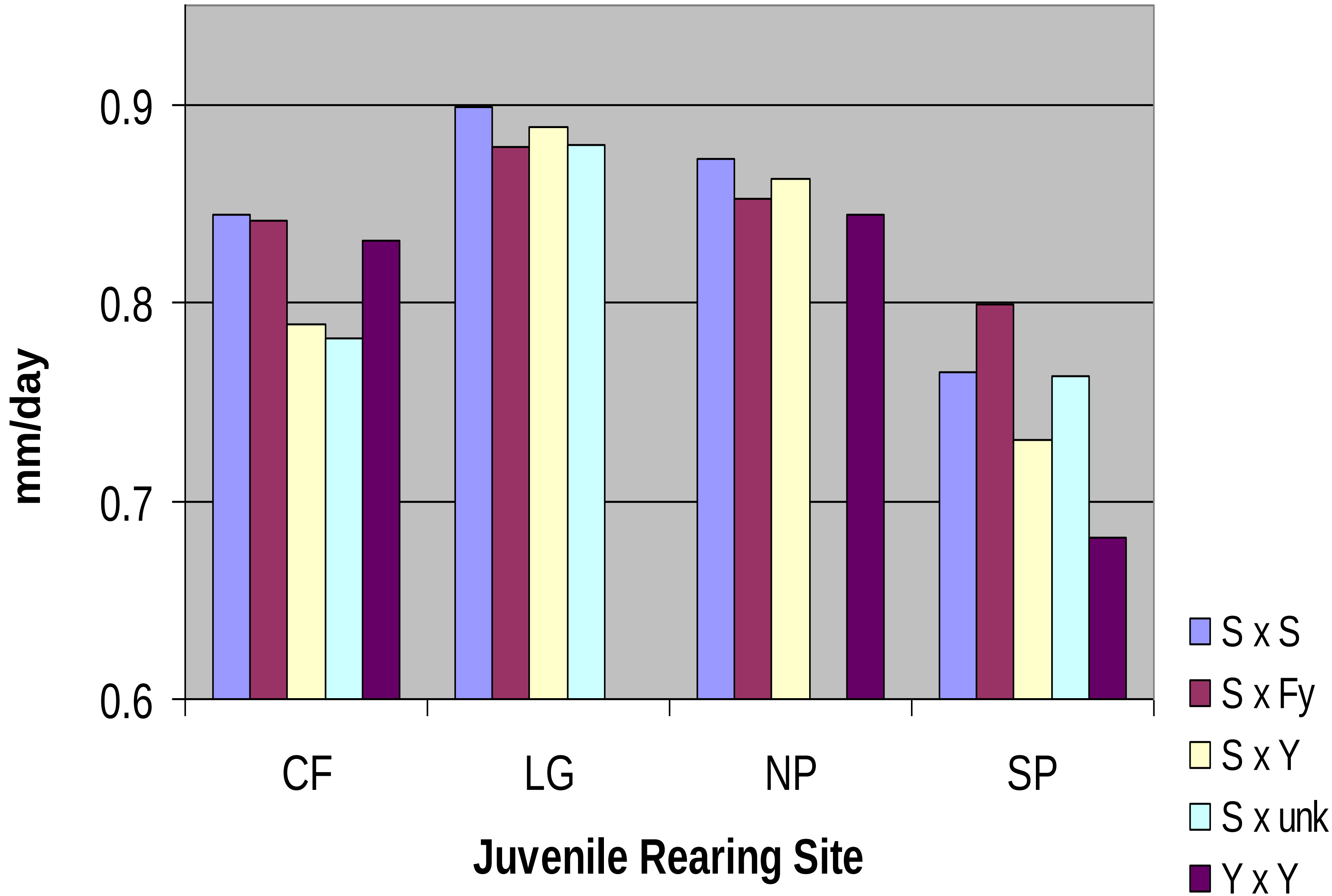


Female FL



Male FL

2007 Juvenile Growth Rate



Some data issues

Parental life history

	SS	mix	YY	FyFy
2007	159	549	37	74
2008	379	352	4	30

Parental origin

2007				
M+F	CF	LG	H-NP	H-SP
H	384	348	257	256
?	26	48	9	19
W	66	84	34	107

2008						
M+F	CF	LG	H-NP	H-SP	NLE	NLW
H	236	229	219	221	262	211
?	8	2	7	17	15	6
W	14	9	20	26	5	23

Model fitting

df	Delta AIC	
31	0	[Year * Site] + FFL + MFL + [FLH * MLH]
23	6.8	Same but no LH interaction
17	31.6	Best fit with no life history
16	488.3	Best fist only life history

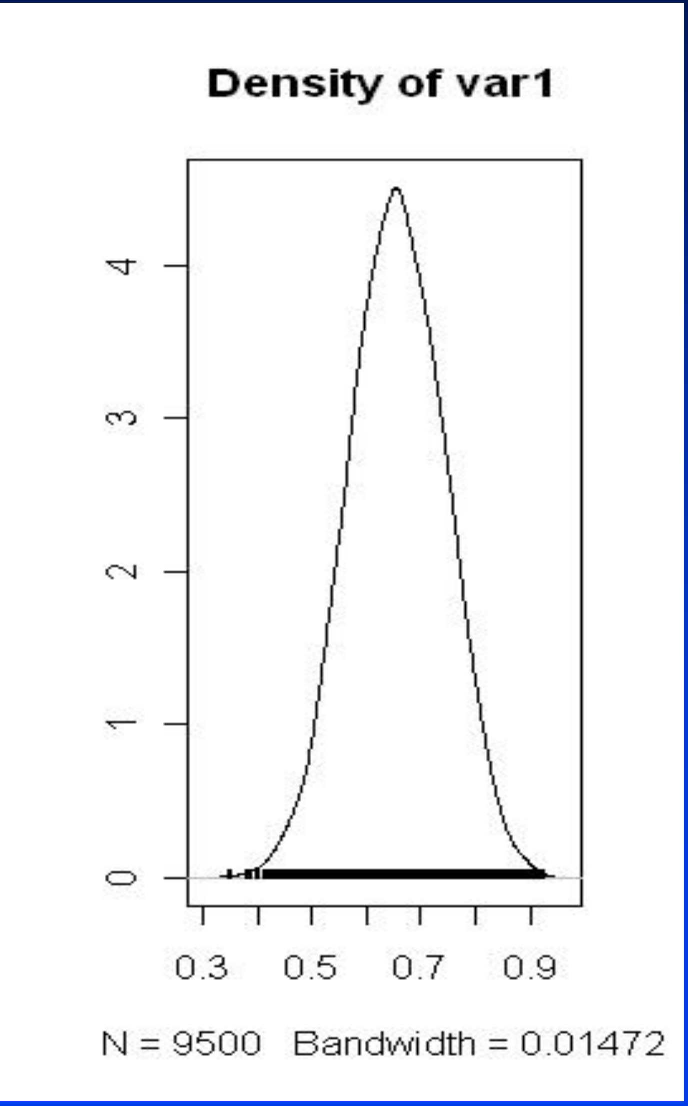
Model fitting (2007+2008 data)

df	delta AIC	
31	0	[Year * Site] + FFL + MFL + [FLH * MLH]
23	6.8	Same but no life history interaction
17	31.6	Best fit without life history
16	488.3	Best fit only life history

Linear model/Anova summary

		2007	2008	2007+2008
Size	FFL	(+)***	(+)*	(+)***
	MFL	(-)*		
Origin			F=W (+)*	
Year			2008(-)***	
Life	Y x Y	(-)** n=37	(+)* n=4	(-) NS
history	Y x S	(-)* n=40		
	S x Y	(-)** n=75		(-)*
	S x ?	(-)** n=48		(-)*
	S x Fy	(-)** n=126		(-)**
	Fy x S	(+)* n=153	(+)*	
	Fy x Fy	(+)P=0.09 n=74	(+)*** n=30	(+)***

Heritability



Broad sense heritability

$$H^2 = V_G/V_P$$

2007	0.67
2008	0.86

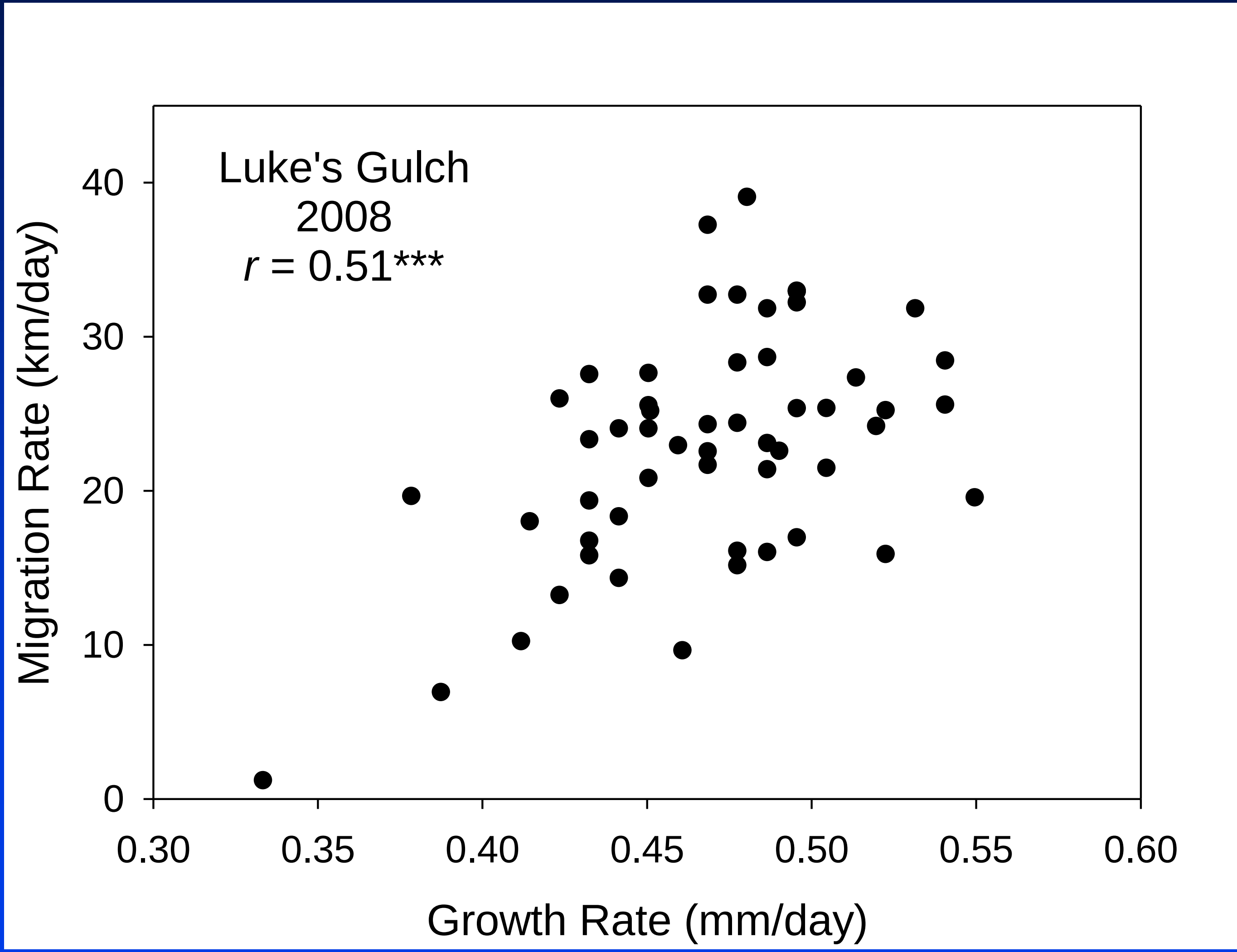
Effects of spawn date?

		Mean Spawn Date
Females		
	Y	320
	S	322
	Unk	319
	Fy	326
Males		
	Y	319
	S	324
	Unk	322
	Fy	323

PIT-tag data

Migration rate x growth rate

	2007	2008
LG	0.24	0.51
CF	0.37	0.41
NP	0.43	0.16
SP	0.16	0.35
LVE		-0.08
LVW		-0.03



PIT-tag data

			%Detect	Distance	Rate
2007	Female	Y	28.6	287.4	11.4
		S	**35.5**	**319.5**	10.6
		Fy	30.6	263.8	9.1
	Male	Y	33.3	325.5	10.9
		S	32.2	294.2	10.2
		Fy	32.5	286.5	9.1
2008	Female	Y	51.4	224.2	12.0
		S	41.3	**279.0**	**14.8**
		Fy	43.3	252.1	11.4
	Male	Y	33.9	268.9	12.2
		S	**43.1**	**270.1**	**13.7**
		Fy	39.8	258.2	13.3

Summary

Subyearling parents generally produce faster growing offspring than do yearling parents

Heritability of juvenile growth rate appears to be high

Juveniles that grow faster tend to migrate farther and faster

Parental life history has a weak effect on offspring migration

Unexpected forced-yearling effect

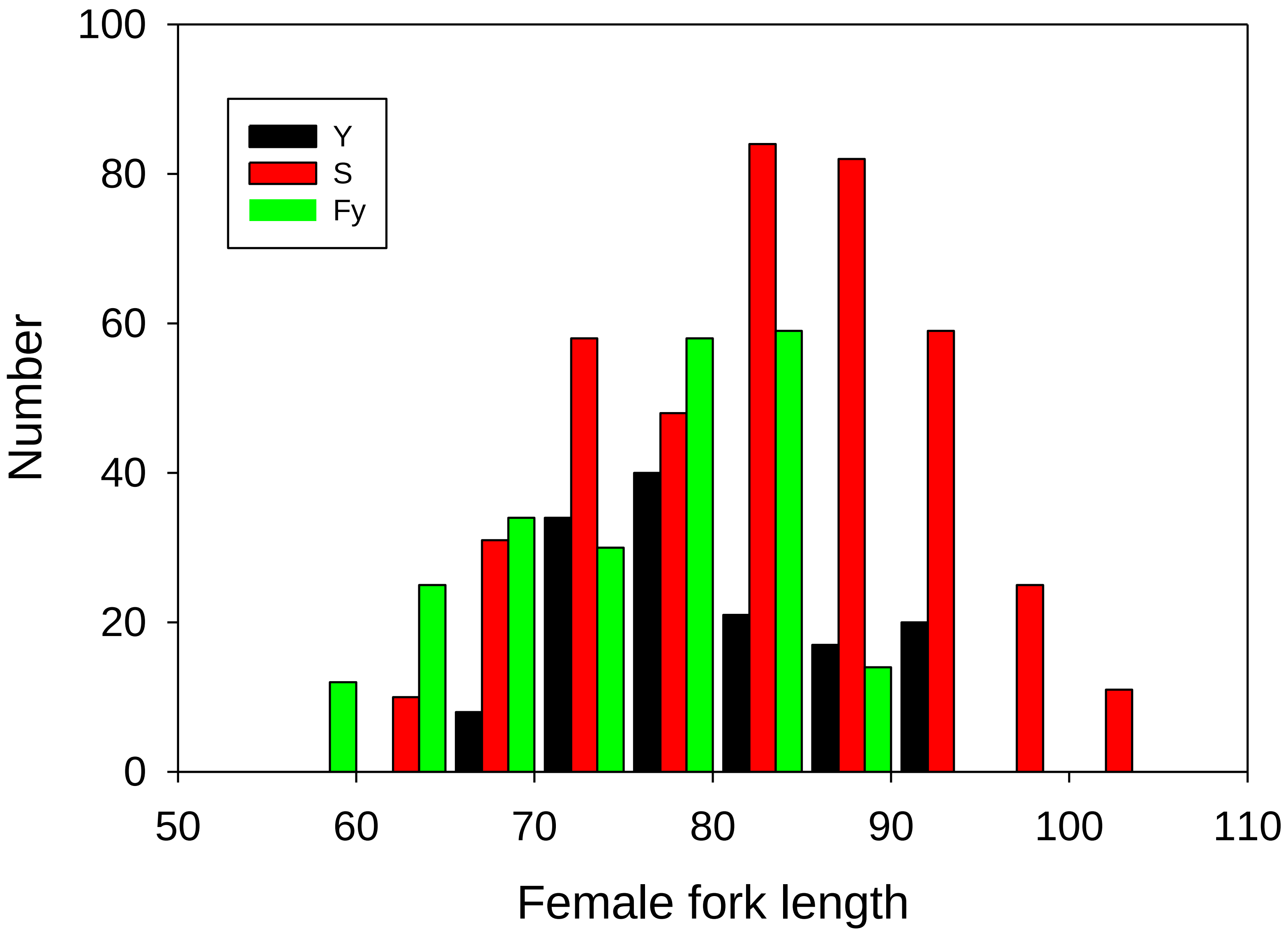
Parents who were forced yearlings produced fastest-growing offspring

= trans-generational effect of hatchery rearing

The effect itself might be due entirely to phenotypic plasticity

However, altered life histories of offpsring expose them to different selective regimes and can have evolutionary consequences

2007 data


Y
S
Fy
Number
0
20
40
60
80
100
50
60
70
80
90
100
110
Female fork length

Thanks

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